ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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          RAW SEQUENCE LISTING                    DATE: 01/11/2001
          PATENT APPLICATION: US/09/674,195       TIME: 17:17:37

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          Output Set: N:\CRF3\01112001\I674195.raw

   4  <110> APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, AS REPRESENTED BY THE
   5        DEPARTMENT OF HEALTH AND HUMAN SERVICES CENTERS FOR DISEASE CONTROL AND
   6        PREVENTION
   7        ZANCOPE-OLIVEIRA, ROSALY M.
   8        LOTT, TIMOTHY J.
   9        MAYER, LEONARD W.
  10        REISS, ERROL
  11        DEEPE, JR., GEORGE S.
  13  <120> TITLE OF INVENTION: NUCLEIC ACIDS OF THE M ANTIGEN GENE OF
  14        HISTOPLASMA CAPSULATUM, ISOLATED AND RECOMBINANTLY-PRODUCED
  15        ANTIGENS, VACCINES AND ANTIBODIES, METHODS AND KITS FOR
  16        DETECTING HISTOPLASMOSIS
  19  <130> FILE REFERENCE: 65798 / US
  21  <140> CURRENT APPLICATION NUMBER: US/09/674,195
  22  <141> CURRENT FILING DATE: 2000-10-26
  24  <150> PRIOR APPLICATION NUMBER: U.S. 60/083,676
  25  <151> PRIOR FILING DATE: 1998-04-30
  27  <150> PRIOR APPLICATION NUMBER: PCT/US99/09151
  28  <151> PRIOR FILING DATE: 1999-04-27
  30  <160> NUMBER OF SEQ ID NOS: 13
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RAW SEQUENCE LISTING   DATE: 01/11/2001
PATENT APPLICATION: US/09/674,195   TIME: 17:17:37

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102   tatagataaa acctgaacga tttagcccct gttggggggaa ataggggtta gggggcgag   3780
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W--> 94

(handwritten) → see item 10 on Erra Summary Sheet

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114  Ser Asp Pro Thr Asp Gln Phe Leu Ser Lys Phe Tyr Ile Asp Asp Glu
115              20                  25                  30
116  Gln Ser Val Leu Thr Thr Asp Val Gly Gly Pro Ile Glu Asp Gln His
117          35                  40                  45
118  Ser Leu Lys Ala Gly Asn Arg Gly Pro Thr Leu Leu Glu Asp Phe Ile
119      50                  55                  60
120  Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg Val Pro Glu Arg
121  65                  70                  75                  80
122  Ala Val His Ala Arg Gly Ala Gly Ala His Gly Val Phe Thr Ser Tyr
123              85                  90                  95
124  Asn Asn Trp Ser Asn Ile Thr Ala Ala Ser Phe Leu Asn Ala Ala Gly
125              100                 105                 110
126  Lys Gln Thr Pro Val Phe Val Arg Phe Ser Thr Val Ala Gly Ser Arg
127          115                 120                 125
128  Gly Ser Val Asp Ser Ala Arg Asp Ile His Gly Phe Ala Thr Arg Leu
129      130                 135                 140
130  Tyr Thr Asp Glu Gly Asn Phe Asp Ile Val Gly Asn Asn Val Pro Val
131  145                 150                 155                 160
132  Phe Phe Ile Gln Asp Ala Ile Gln Phe Pro Asp Leu Ile His Ala Val
133              165                 170                 175
134  Lys Pro Gln Pro Asp Ser Glu Ile Pro Gln Ala Ala Thr Ala His Asp
135              180                 185                 190
136  Thr Ala Trp Asp Phe Leu Ser Gln Gln Pro Ser Ser Leu His Ala Leu
137          195                 200                 205
138  Phe Trp Ala Met Ser Gly His Gly Ile Pro Arg Ser Met Arg His Val
139      210                 215                 220
140  Asp Gly Trp Gly Val His Thr Phe Arg Leu Val Thr Asp Glu Gly Asn
141  225                 230                 235                 240
142  Ser Thr Leu Val Lys Phe Arg Trp Lys Thr Leu Gln Gly Arg Ala Gly
143              245                 250                 255
144  Leu Val Trp Glu Glu Ala Gln Ala Leu Gly Gly Lys Asn Pro Asp Phe
145              260                 265                 270
146  His Arg Glu Asp Leu Trp Asp Ala Ile Glu Ser Gly Arg Tyr Pro Glu
147          275                 280                 285
148  Trp Glu Leu Gly Phe Gln Leu Val Asn Glu Ala Asp Gln Ser Lys Phe
149      290                 295                 300
150  Asp Phe Asp Leu Leu Asp Pro Thr Lys Ile Ile Pro Glu Glu Leu Val
151  305                 310                 315                 320
152  Pro Phe Thr Pro Ile Gly Lys Met Val Leu Asn Arg Asn Pro Lys Ser
153              325                 330                 335
154  Tyr Phe Ala Glu Thr Glu Gln Ile Met Phe Gln Pro Gly His Val Val
155              340                 345                 350
156  Arg Gly Ile Asp Phe Thr Asp Asp Pro Leu Leu Gln Gly Arg Leu Tyr
157          355                 360                 365
158  Ser Tyr Leu Asp Thr Gln Leu Asn Arg His Gly Gly Pro Asn Phe Glu
159      370                 375                 380
160  Gln Leu Pro Ile Asn Arg Pro Arg Ile Pro Phe His Asn Asn Asn Arg
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/674,195

DATE: 01/11/2001
TIME: 17:17:37

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166  Asn Arg Gly Phe Phe Thr Ala Pro Gly Arg Met Val Asn Gly Pro Leu
167              435                      440                      445
168  Val Arg Glu Leu Ser Pro Ser Phe Asn Asp Val Trp Ser Gln Pro Arg
169          450                      455                      460
170  Leu Phe Tyr Asn Ser Leu Thr Val Phe Glu Lys Gln Phe Leu Val Asn
171  465                      470                      475                      480
172  Ala Met Arg Phe Glu Asn Ser His Val Arg Ser Glu Thr Val Arg Lys
173                      485                      490                      495
174  Asn Val Ile Ile Gln Leu Asn Arg Val Asp Asn Asp Leu Ala Arg Arg
175                  500                      505                      510
176  Val Ala Leu Ala Ile Gly Val Glu Pro Pro Ser Pro Asp Pro Thr Phe
177              515                      520                      525
178  Tyr His Asn Lys Ala Thr Val Pro Ile Gly Thr Phe Gly Thr Asn Leu
179      530                      535                      540
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VERIFICATION SUMMARY   DATE: 01/11/2001
PATENT APPLICATION: US/09/674,195   TIME: 17:17:38

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        Output Set: N:\CRF3\01112001\I674195.raw

L:21 M:270 C: Current Application Number differs, Replaced Current Application Number
L:22 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:94 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
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L:286 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11

ERROR DETECTED   SUGGESTED CORRECTION   SERIAL NUMBER: 09/674,195

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line...
                                   This may occur if your file was retrieved in a word processor after creating it.
                                   Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped" down to the next line.
                                   This may occur if your file was retrieved in a word processor after creating it.
                                   Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
        Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
                                  Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
                                  As per the rules, each n or Xaa can only represent a single residue.
                                  Please present the maximum number of each residue having variable length and
                                  indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
                                  sequence(s) _____. Normally, PatentIn would automatically generate this section from the
                                  previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
                                  to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
                                  sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
        (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X:
                                  (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
                                  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
                                  This sequence is intentionally skipped

                                  Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
        (NEW RULES)   <210> sequence id number
                                  <400> sequence id number
                                  000

10 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
         (NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
                                  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism   Sequence(s) _____ are missing this mandatory field or its response.
         (NEW RULES)

12 _____ Use of <220>Feature   Sequence(s) _____ are missing the <220>Feature and associated headings.
         (NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
                                  Please explain source of genetic material in <220> to <223> section.
                                  (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
                                  file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
                                  Instead, please use "File Manager" or any other means to copy file to floppy disk.